



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,945

DATE: 08/14/2002

TIME: 11:43:30

Input Set : A:\10624092999.txt
 Output Set: N:\CRF4\08142002\J009945.raw

3 <110> APPLICANT: Thomsen, Gerald
 4 Wrana, Jeffery
 6 <120> TITLE OF INVENTION: ANTAGONISTS OF BMP AND TGF-BETA SIGNALING PATHWAYS
 8 <130> FILE REFERENCE: 10624-092
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/009,945
 C--> 10 <141> CURRENT FILING DATE: 2002-06-21
 10 <160> NUMBER OF SEQ ID NOS: 13
 12 <170> SOFTWARE: PatentIn version 3.1
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 2172
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 19 <220> FEATURE:
 20 <223> OTHER INFORMATION: Human Smurf1
 22 <400> SEQUENCE: 1
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 24 gacttcttca ggctccctga ccctttgca aagattgtcg tggatgggtc tggcagtgc 120
 25 cactcaaccc acactgtgaa aaacacattg gaccggaaat ggaaccagca ctatgtatcta 180
 26 tatgttggga aaacggattc gataaccatt agcgtgtgga accataagaa aattcacaag 240
 27 aaacaggggag ctggcttcct gggctgtgtg cggctgctc ccaatggcat cagcagattt 300
 28 aaagataaccg gataccagcg tttggatcta tgcaaaactaa acccctcaga tactgtatgc 360
 29 gttcgtggcc agatagtgg tcaatgttacag acacgagaca gaataggaaac cggcggctcg 420
 30 gtgggtggact gcagaggact gtttagaaaaat gaaggAACGG ttatgttgaaga ctccggggct 480
 31 gggaggccgc tcagctgctt catggagggaa ccagccccctt acacagatag caccgggtct 540
 32 gctgctggag gagggattt cagggtcg tggatccctt gtcaagatca aagacttcag 600
 33 gcacagcgcc ttcgaaaccc tggatgtgcg gtttactac agacgccccca gaaccgacca 660
 34 cacggccacc agtccccggaa actccccggaa ggctacgaac aaagaacaac agtccagggc 720
 35 caagtttact ttttgcatac acagactgaa gtttgcacgt ggcacgaccc caggatacca 780
 36 agagaccta acagtgtgaa ctgtgtatggaa cttggaccac tgccggccagg ctggaaatgc 840
 37 agaagtacag ttctggag gatataatttt gtagatcata ataaccgaac aaccctgttt 900
 38 acagacccaa ggttacacca catcatgaat caccatgcc aactcaaggaa gcccagccag 960
 39 ccgctgcccc tggatgtgaa gggctctctg gaggacgagg agcttccctgc ccagagatac 1020
 40 gaaagagatc tagtccagaa gctgaaatgc ctcagacacg aactgtcgt tcagcagccc 1080
 41 caagctggcc attggccat cgaagtgtcc agagaagaaa tctttggatggaa gtcttaccgc 1140
 42 cagataatga agatgcgacc gaaagacttgg aaaaaacggc tggatgtgaa attccgtggg 1200
 43 gaagaagggtt tggattacgg tggatgtggc agggatgtgc tttacttgcgt gtggcatgaa 1260
 44 atgctgaatc ttattacgg gctcttccag tatttacgg acaatattttt catgttgcaa 1320
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 46 atcatggggc tggatgtgtt ccatggacac tacatcaacg gggggcttac agtgccttc 1440
 47 tacaaggcgc tggatgtggaa gcccatccag ctctcagatc tggatgtgtt ggaccacagg 1500
 48 ctgcataaga gcttgggtgt gatcttagag aacgacatca cgcctgtact ggaccacacc 1560
 49 ttctgcgtgg aacacaacgc ttccggccgg atcctgcagc atgaaactgaa acccaatggc 1620
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ENTERED

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51 aggttatga gaggaatcga agcccagttc ttagctctgc agaaggggtt caatgagctc 1740
 52 atccctcaac atctgctgaa gcctttgac cagaaggaac tggagctgat cataggcgcc 1800
 53 ctggataaaa tagacttcaa cgactggaa tcgaacacgc ggctgaagca ctgtgtggcc 1860
 54 gacagcaaca tcgtcggtg gttctggcaa gcgggtggaga cgttcgatga agaaaggagg 1920
 55 gccaggctcc tgcagttgt gactgggtcc acgcgagtcc cgctccaagg cttcaaggct 1980
 56 ttgcaagggtt ctacaggcgc ggcagggccc cggctgttca ccatccacct gatagacgcg 2040
 57 aacacagaca accttccgaa ggcccatacc tgcttaacc ggatcgacat tccaccatat 2100
 58 gagtccatag agaagctcta cgagaagctg ctgacagcog tggaggagac ctgcgggttt 2160
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 62 <211> LENGTH: 723
 63 <212> TYPE: PRT
 64 <213> ORGANISM: Homo sapiens
 66 <220> FEATURE:
 67 <223> OTHER INFORMATION: Human Smurf1
 69 <400> SEQUENCE: 2
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 73 Leu Ala Lys Lys Asp Phe Phe Arg Leu Pro Asp Pro Phe Ala Lys Ile
 74 20 25 30
 76 Val Val Asp Gly Ser Gly Gln Cys His Ser Thr Asp Thr Val Lys Asn
 77 35 40 45
 79 Thr Leu Asp Pro Lys Trp Asn Gln His Tyr Asp Leu Tyr Val Gly Lys
 80 50 55 60
 82 Thr Asp Ser Ile Thr Ile Ser Val Trp Asn His Lys Lys Ile His Lys
 83 65 70 75 80
 85 Lys Gln Gly Ala Gly Phe Leu Gly Cys Val Arg Leu Leu Ser Asn Ala
 86 85 90 95
 88 Ile Ser Arg Leu Lys Asp Thr Gly Tyr Gln Arg Leu Asp Leu Cys Lys
 89 100 105 110
 91 Leu Asn Pro Ser Asp Thr Asp Ala Val Arg Gly Gln Ile Val Val Ser
 92 115 120 125
 94 Leu Gln Thr Arg Asp Arg Ile Gly Thr Gly Gly Ser Val Val Asp Cys
 95 130 135 140
 97 Arg Gly Leu Leu Glu Asn Glu Gly Thr Val Tyr Glu Asp Ser Gly Pro
 98 145 150 155 160
 100 Gly Arg Pro Leu Ser Cys Phe Met Glu Glu Pro Ala Pro Tyr Thr Asp
 101 165 170 175
 103 Ser Thr Gly Ala Ala Ala Gly Gly Asn Cys Arg Phe Val Glu Ser
 104 180 185 190
 106 Pro Ser Gln Asp Gln Arg Leu Gln Ala Gln Arg Leu Arg Asn Pro Asp
 107 195 200 205
 109 Val Arg Gly Ser Leu Gln Thr Pro Gln Asn Arg Pro His Gly His Gln
 110 210 215 220
 112 Ser Pro Glu Leu Pro Glu Gly Tyr Glu Gln Arg Thr Thr Val Gln Gly
 113 225 230 235 240
 115 Gln Val Tyr Phe Leu His Thr Gln Thr Gly Val Ser Thr Trp His Asp
 116 245 250 255
 118 Pro Arg Ile Pro Arg Asp Leu Asn Ser Val Asn Cys Asp Glu Leu Gly

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119	260	265	270	
121	Pro Leu Pro Pro Gly Trp Glu Val Arg Ser Thr Val Ser Gly Arg Ile			
122	275	280	285	
124	Tyr Phe Val Asp His Asn Asn Arg Thr Thr Gln Phe Thr Asp Pro Arg			
125	290	295	300	
127	Leu His His Ile Met Asn His Gln Cys Gln Leu Lys Glu Pro Ser Gln			
128	305	310	315	320
130	Pro Leu Pro Leu Pro Ser Glu Gly Ser Leu Glu Asp Glu Glu Leu Pro			
131	325	330	335	
133	Ala Gln Arg Tyr Glu Arg Asp Leu Val Gln Lys Leu Lys Val Leu Arg			
134	340	345	350	
136	His Glu Leu Ser Leu Gln Gln Pro Gln Ala Gly His Cys Arg Ile Glu			
137	355	360	365	
139	Val Ser Arg Glu Glu Ile Phe Glu Glu Ser Tyr Arg Gln Ile Met Lys			
140	370	375	380	
142	Met Arg Pro Lys Asp Leu Lys Lys Arg Leu Met Val Lys Phe Arg Gly			
143	385	390	395	400
145	Glu Glu Gly Leu Asp Tyr Gly Gly Val Ala Arg Glu Trp Leu Tyr Leu			
146	405	410	415	
148	Leu Cys His Glu Met Leu Asn Pro Tyr Tyr Gly Leu Phe Gln Tyr Ser			
149	420	425	430	
151	Thr Asp Asn Ile Tyr Met Leu Gln Ile Asn Pro Asp Ser Ser Ile Asn			
152	435	440	445	
154	Pro Asp His Leu Ser Tyr Phe His Phe Val Gly Arg Ile Met Gly Leu			
155	450	455	460	
157	Ala Val Phe His Gly His Tyr Ile Asn Gly Gly Phe Thr Val Pro Phe			
158	465	470	475	480
160	Tyr Lys Gln Leu Leu Gly Lys Pro Ile Gln Leu Ser Asp Leu Glu Ser			
161	485	490	495	
163	Val Asp Pro Glu Leu His Lys Ser Leu Val Trp Ile Leu Glu Asn Asp			
164	500	505	510	
166	Ile Thr Pro Val Leu Asp His Thr Phe Cys Val Glu His Asn Ala Phe			
167	515	520	525	
169	Gly Arg Ile Leu Gln His Glu Leu Lys Pro Asn Gly Arg Asn Val Pro			
170	530	535	540	
172	Val Thr Glu Glu Asn Lys Lys Glu Tyr Val Arg Leu Tyr Val Asn Trp			
173	545	550	555	560
175	Arg Phe Met Arg Gly Ile Glu Ala Gln Phe Leu Ala Leu Gln Lys Gly			
176	565	570	575	
178	Phe Asn Glu Leu Ile Pro Gln His Leu Leu Lys Pro Phe Asp Gln Lys			
179	580	585	590	
181	Glu Leu Glu Leu Ile Ile Gly Gly Leu Asp Lys Ile Asp Leu Asn Asp			
182	595	600	605	
184	Trp Lys Ser Asn Thr Arg Leu Lys His Cys Val Ala Asp Ser Asn Ile			
185	610	615	620	
187	Val Arg Trp Phe Trp Gln Ala Val Glu Thr Phe Asp Glu Glu Arg Arg			
188	625	630	635	640
190	Ala Arg Leu Leu Gln Phe Val Thr Gly Ser Thr Arg Val Pro Leu Gln			
191	645	650	655	

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193 Gly Phe Lys Ala Leu Gln Gly Ser Thr Gly Ala Ala Gly Pro Arg Leu
194 660 665 670
196 Phe Thr Ile His Leu Ile Asp Ala Asn Thr Asp Asn Leu Pro Lys Ala
197 675 680 685
199 His Thr Cys Phe Asn Arg Ile Asp Ile Pro Pro Tyr Glu Ser Tyr Glu
200 690 695 700
202 Lys Leu Tyr Glu Lys Leu Leu Thr Ala Val Glu Glu Thr Cys Gly Phe
203 705 710 715 720
205 Ala Val Glu
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 2247
210 <212> TYPE: DNA
211 <213> ORGANISM: Homo sapiens
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Human Smurf2
216 <400> SEQUENCE: 3
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218 gcaaaaaacc tggtaaaaaa ggatttttc cgacttcctg atccatttgc taaggtggtg 120
219 gttgatggat ctgggcaatg ccatttctaca gatactgtga agaatacgt tgatccaaag 180
220 tggaaatcagc attatgacct gtatatttga aagtctgatt cagttacatc cagtgtatgg 240
221 aatcacaaga agatccataa gaaacaaggt gctggatttc tcgggttgc tcgtttctt 300
222 tccaaatgcca tcaaccgcct caaagacact gtttgcataa ggttggattt atgcaaaactc 360
223 gggccaaatg acaatgatac agtttaggaa cagatagtag taagtcttca gtccagagac 420
224 cgaataggca caggaggaca agttgtggac tgcagtcgtt tatttgcataa cgatttacca 480
225 gacggctgg aaaaaaggag aaccgcctt ggaagaatcc agtatctaaa ccataataaca 540
226 agaactacgc aatgggagcg cccaaacacga ccgcattccg aatattcttag ccctggcaga 600
227 cctcttagct gctttgttga tgagaacact ccaatttagt gaacaaatgg tgcaacatgt 660
228 ggacagtctt cagatcccg gctggcagag aggagagtca ggtcacaacg acatagaaat 720
229 tacatgagca gaacacattt acatacttcc ccagacctac cagaaggcta tgaacagagg 780
230 acaacgcaac aaggccagg tattttttaa catacacaaga ctgggtgtg cacatggcat 840
231 gatccaagag tgcccaggaa tcttagcaac atcaatttgc aagagcttgc tccattgcct 900
232 cctggatggg agatccgtaa tacggcaaca ggcagagttt atttcgttgc ccataacaac 960
233 agaacaacac aatttacaga tcctcggtc tctgtcaact tgcatttagt tttaatcg 1020
234 cagaaccaat tgaaagacca acagcaacag caagtggat cgttatgtcc tgatgacaca 1080
235 gaatgcctga cagtcggcaag gtacaagcga gacctgggtc agaaactaaa aattttgcgg 1140
236 caagaacttt cccaaacaaca gcctcagcga ggtcatttgc gcatttgcgtt ttccaggaa 1200
237 gagatttttgc aggaatcata tcgacaggc atgaaaatgc gaccaaaaaga tcttgcgg 1260
238 cgattaaatgc taaaatttcg tggagaagaa ggccttgcgt atggaggcgt tgccaggaa 1320
239 tgggtgtatc tcttgcatac tgaaatgttgc aatccataact atggccttcc ccagtattca 1380
240 agagatgata ttatatacatt gcagatcaat cctgatttgc cagttaatcc ggaacattta 1440
241 tccttatttcc actttgtgg acgaaataatgc ggaatggcgt tggttcatgg acattatatt 1500
242 gatggtgggtt tcacatttgc tttttataag caatttgcgtt ggaagtcaat taccttggat 1560
243 gacatggagt tagtagatcc ggatcttcac aacagtttag tggatgttgc tgagaatgtat 1620
244 attacagggtt ttttggacca tacatttgcgtt gttgaaacata atgcataatgg tggaaatttt 1680
245 cagcatgaac taaaacccaaa tggcaaaaatgc atccctgttgc atgaaagaaaa taaaaaaagaa 1740
246 tatgtcaggc tctatgtgaa ctggagatcc ttacggaggca ttggaggcgttca attcttggct 1800
247 ctgcagaaag gatataatgc agtaatttccca caacatctgc tgaagacatt tgatgagaag 1860
248 gagtttagagc tcatttatttgc tggacttggaa aagatagatgc ttaatgtactg gaaggtaaac 1920
249 accccgtttaa aacactgtac accagacagc aacatttgc aatgggttgc gaaagctgtg 1980

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250 gagtttttg atgaagagcg acgagcaaga ttgcttcagt ttgtgacagg atccctcga 2040
251 gtgcctctgc agggcttcaa agcattgcaa ggtgctgcag gccccgagact ctttaccata 2100
252 caccagattg atgcctgcac taacaacctg ccgaaagccc acacttgctt caatcgaata 2160
253 gacattccac cctatgaaaag ctatgaaaag ctatatgaaa agctgctaac agccattgaa 2220
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257 <211> LENGTH: 748
258 <212> TYPE: PRT
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Human Smurf1
264 <400> SEQUENCE: 4
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268 Thr Val Leu Cys Ala Lys Asn Leu Val Lys Lys Asp Phe Phe Arg Leu
269 20 25 30
271 Pro Asp Pro Phe Ala Lys Val Val Asp Gly Ser Gly Gln Cys His
272 35 40 45
274 Ser Thr Asp Thr Val Lys Asn Thr Leu Asp Pro Lys Trp Asn Gln His
275 50 55 60
277 Tyr Asp Leu Tyr Ile Gly Lys Ser Asp Ser Val Thr Ile Ser Val Trp
278 65 70 75 80
280 Asn His Lys Lys Ile His Lys Lys Gln Gly Ala Gly Phe Leu Gly Cys
281 85 90 95
283 Val Arg Leu Leu Ser Asn Ala Ile Asn Arg Leu Lys Asp Thr Gly Tyr
284 100 105 110
286 Gln Arg Leu Asp Leu Cys Lys Leu Gly Pro Asn Asp Asn Asp Thr Val
287 115 120 125
289 Arg Gly Gln Ile Val Val Ser Leu Gln Ser Arg Asp Arg Ile Gly Thr
290 130 135 140
292 Gly Gly Gln Val Val Asp Cys Ser Arg Leu Phe Asp Asn Asp Leu Pro
293 145 150 155 160
295 Asp Gly Trp Glu Glu Arg Arg Thr Ala Ser Gly Arg Ile Gln Tyr Leu
296 165 170 175
298 Asn His Ile Thr Arg Thr Thr Gln Trp Glu Arg Pro Thr Arg Pro Ala
299 180 185 190
301 Ser Glu Tyr Ser Ser Pro Gly Arg Pro Leu Ser Cys Phe Val Asp Glu
302 195 200 205
304 Asn Thr Pro Ile Ser Gly Thr Asn Gly Ala Thr Cys Gly Gln Ser Ser
305 210 215 220
307 Asp Pro Arg Leu Ala Glu Arg Arg Val Arg Ser Gln Arg His Arg Asn
308 225 230 235 240
310 Tyr Met Ser Arg Thr His Leu His Thr Pro Pro Asp Leu Pro Glu Gly
311 245 250 255
313 Tyr Glu Gln Arg Thr Thr Gln Gln Gly Gln Val Tyr Phe Leu His Thr
314 260 265 270
316 Gln Thr Gly Val Ser Thr Trp His Asp Pro Arg Val Pro Arg Asp Leu
317 275 280 285
319 Ser Asn Ile Asn Cys Glu Glu Leu Gly Pro Leu Pro Pro Gly Trp Glu

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; Xaa Pos. 3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,9,10,11,12,13